

REMARKS

Claims 5 and 35-40 are pending. Claims 5 and 36-40 have been amended to reference amino acid residues 1-686 of SEQ ID NO:2 instead of SEQ ID NO:1.

Applicants submit a paper copy and a computer readable form of a Sequence Listing. The content of the paper and of the computer readable form is the same. The prior sequence listing incorrectly listed the first amino of the CDS as the first amino acid of the mature polypeptide. The new sequence listing corrects this error. Accordingly, this submission contains no new matter.

Applicants also submit a formal drawing for Figure 1, responsive to the Notice of Draftperson's Patent Drawing Review.

It is respectfully submitted that the present amendment presents no new issues or new matter and places this case in condition for allowance. Reconsideration of the application in view of the above amendments and the following remarks is requested.

I. The Rejection of Claims 5 and 35-40 under 35 U.S.C. 112

Claims 5 and 35-40 are rejected under 35 U.S.C. 112, as allegedly lacking adequate written description support. The Examiner contends that there is no disclosure for a three-dimensional crystal structure of SEQ ID NO:1, but states that there is a disclosure for a three dimensional structure of SEQ ID NO:2.

As amended, the claims now reference the three-dimensional structure of amino acid residues 1-686 of SEQ ID NO:2 instead of SEQ ID NO:1.

For the foregoing reasons, Applicants submit that the claims overcome this rejection under 35 U.S.C. 112. Applicants respectfully request reconsideration and withdrawal of the rejection.

II. The Rejection of Claims 5 and 35-40 under 35 U.S.C. 112

Claims 5 and 35-40 are rejected under 35 U.S.C. 112, as allegedly non-enabled. The Examiner acknowledges that the specification is enabled for a variant of an alpha-amylase using the three dimensional structure of SEQ ID NO:2.

As amended, the claims now reference the three-dimensional structure of amino acid residues 1-686 of SEQ ID NO:2.

For the foregoing reasons, Applicants submit that the claims overcome this rejection under 35 U.S.C. 112. Applicants respectfully request reconsideration and withdrawal of the rejection.

III. The Rejection of Claims 5 and 35-40 under 35 U.S.C. 112

Claims 5 and 35-40 are rejected under 35 U.S.C. 112, as allegedly indefinite. The Examiner state that it is unclear whether applicants refer to SEQ ID NO:1 as the nucleic acid sequence or as an amino acid sequence.

As amended, the claims now reference the three-dimensional structure of the amino acid sequence of amino acid residues 1-686 of SEQ ID NO:2.

For the foregoing reasons, Applicants submit that the claims overcome this rejection under 35 U.S.C. 112. Applicants respectfully request reconsideration and withdrawal of the rejection.

IV. Conclusion

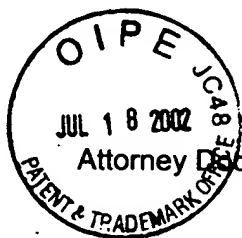
In view of the above, it is respectfully submitted that all claims are in condition for allowance. Early action to that end is respectfully requested. The Examiner is hereby invited to contact the undersigned by telephone if there are any questions concerning this amendment or application.

Respectfully submitted,

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In re Application of: Cherry et al.

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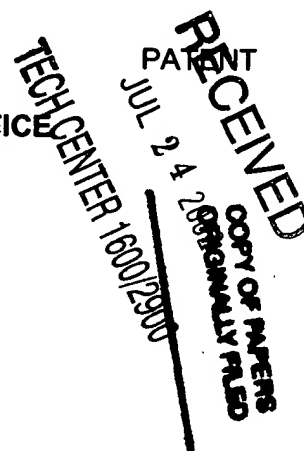
Serial No.: 09/607,142

Group Art Unit: 1631

Filed: June 29, 2000

Examiner: Mahatan, C.

For: Maltogenic Alpha-Amylase Variants



VERSION WITH MARKINGS TO SHOW CHANGES MADE

Sir:

Below is a marked-up version of the amendments made in the accompanying amendment.

IN THE CLAIMS:

The claims have been amended as follows:

5. (Twice Amended.) A method of constructing a variant of a parent maltogenic alpha-amylase, wherein said parent maltogenic alpha-amylase has an amino acid sequence which is at least 70% identical to [SEQ ID NO:1] amino acid residues 1-686 of SEQ ID NO:2, which method comprises:

- a) modeling the parent alpha-amylase on the three-dimensional structure of [SEQ ID NO: 1] amino acid residues 1-686 of SEQ ID NO:2 depicted in the Appendix to produce a three-dimensional structure of the parent alpha-amylase;
- b) identifying an amino acid residue which is within 15 Å from an active site residue of the parent amylase in the three-dimensional structure of said parent, and which is involved in electrostatic or hydrophobic interactions with an active site residue;
- c) substituting said amino acid residue with another amino acid residue which changes the electrostatic and/or hydrophobic surroundings of an active site residue, and which can be accommodated in the structure;
- d) optionally repeating steps b) and c) recursively;
- e) optionally, making alterations each of which is an insertion, a deletion or a substitution of an amino acid residue at one or more positions other than c),
- f) preparing the variant resulting from steps a) – e);
- g) testing the pH dependent activity of said variant; and

- h) optionally repeating steps a) - g) recursively; and
- i) selecting a variant having an altered pH dependent activity as compared to the parent amylase.

35. (Unchanged.) The method of claim 5, wherein said b) involves identifying an amino acid residue which is within 10 Å from an active site residue of the parent amylase in the three-dimensional structure of said parent, and which is involved in electrostatic or hydrophobic interactions with an active site residue.

36. (Amended.) The method of claim 5 or 35, wherein said parent maltogenic alpha-amylase at least 80% identical to [SEQ ID NO:1] amino acid residues 1-686 of SEQ ID NO:2.

37. (Amended.) The method of claim 5 or 35, wherein said parent maltogenic alpha-amylase is at least 90% identical to [SEQ ID NO:1] amino acid residues 1-686 of SEQ ID NO:2.

38. (Amended.) The method of claim 5 or 35, wherein said parent maltogenic alpha-amylase is at least 95% identical to [SEQ ID NO:1] amino acid residues 1-686 of SEQ ID NO:2.

39. (Amended.) The method of claim 5 or 35, wherein said parent maltogenic alpha-amylase is at least 98% identical to [SEQ ID NO:1] amino acid residues 1-686 of SEQ ID NO:2.

40. (Amended.) The method of claim 5 or 35, wherein said parent maltogenic alpha-amylase has the amino acid sequence of [SEQ ID NO:1] amino acid residues 1-686 of SEQ ID NO:2.